



OIPE

RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/084,406

TIME: 09:59:47

Input Set : N:\Crf3\RULE60\10084406.raw

Output Set: N:\CRF3\04112002\J084406.raw

1 <110> APPLICANT: Schwientek, Tilo
 2 Clausen, Henrik
 3 <120> TITLE OF INVENTION: UPD-N-Acetylglucosamine:
 4 Galactose-betal,3-N-Acetylglactosamine-alpha-R / (GlcNAc
 5 to GalNAc) betal,6-N-Acetylglucosamineyltransferase, C2GnT3
 6 <130> FILE REFERENCE: 4503/1G031
 7 <140> CURRENT APPLICATION NUMBER: 10/084,406
 8 <141> CURRENT FILING DATE: 2002-02-25
 9 <150> PRIOR APPLICATION NUMBER: 09/645,192
 10 <151> PRIOR FILING DATE: 2000-08-24
 11 <160> NUMBER OF SEQ ID NOS: 17
 12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 1362
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Human
 18 <400> SEQUENCE: 1

ENTERED

19	atgaagatat	tcaaatgtta	ttttaaacat	accctacagc	agaaagtgttt	catcctgttt	60
20	ttaaccctat	ggctgctctc	tttgttaaag	cttctaaatg	tgagacgact	ctttccgcaa	120
21	aaagacattt	acttggttga	gtactcccta	agtacctcgc	cttttgtaag	aaacagatac	180
22	actcatgtta	aggatgaagt	caggatgaa	gttaactgtt	cgggtatcta	tgaacaggag	240
23	cctttggaaa	ttggaaagag	tctggaaata	agaagaaggg	acatcattga	cttggaggat	300
24	gatgatgttg	tggcaatgac	cagtgtattg	gacattttatc	agactctaag	aggttatgct	360
25	caaaagcttg	tctcaaagga	ggagaaaagc	ttcccaatag	cctattcttt	ggttgtccac	420
26	aaagatgcaa	ttatggttga	aaggcttatc	catgctatat	acaaccagca	caatatttac	480
27	tgcaccatt	atgatcgtaa	ggcacctgat	accttcaaag	ttgccatgaa	caatttagct	540
28	aagtgtctct	ccaatatttt	cattgtcttc	aaattagagg	ctgtggaata	tgccacatt	600
29	tccagactcc	aggtgatatt	aaattgcttg	tgggaccttc	tgaagtcttc	aatccagtgg	660
30	aaatatgtta	tcaacttggtg	tgggcaagat	tttcccctga	agtcaaattt	tgaattggtg	720
31	tcagagttga	aaaaactcaa	tggagcaaat	atgttgga	cggtgaaacc	cccaaacagt	780
32	aaattggaaa	gattcactta	ccatcatgaa	cttagacggg	tgcccttatga	atatgtgaag	840
33	ctaccaataa	ggacaaacat	ctccaaggaa	gcaccccccc	ataacattca	gatatttggt	900
34	ggcagtgtct	attttggttt	aagtcaagca	tttgttaaat	atattttcaa	caactccatc	960
35	gttcaagact	tttttgcttg	gtctaaagac	acatactctc	ctgatgagca	cttttgggct	1020
36	accttgattc	gggttccagg	aatacctggg	gagatttcca	gatcagccca	ggatgtgtct	1080
37	gatctgcaga	gtaagactcg	ccttgctcaag	tggaaattact	atgaaggctt	tttctatccc	1140
38	agttgtactg	gatctcacct	tgaagcgtg	tgtattttatg	gagctgcaga	attaaggtgg	1200
39	cttatcaaag	atggacattg	gtttgcta	aaatttgatt	ctaaggtgga	ccctatcttg	1260
40	attaaatgct	tggcagaaaa	gcttgaagaa	cagcagagag	actggatcac	tttgccctca	1320
41	gaaaagtgtat	ttatggatag	aaatctcact	accacatcat	ga		1362

43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 453
 45 <212> TYPE: PRT

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46 <213> ORGANISM: Human

47 <400> SEQUENCE: 2

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48   Met Lys Ile Phe Lys Cys Tyr Phe Lys His Thr Leu Gln Gln Lys Val
49       1           5           10           15
50   Phe Ile Leu Phe Leu Thr Leu Trp Leu Ser Leu Leu Lys Leu Leu
51       20           25           30
52   Asn Val Arg Arg Leu Phe Pro Gln Lys Asp Ile Tyr Leu Val Glu Tyr
53       35           40           45
54   Ser Leu Ser Thr Ser Pro Phe Val Arg Asn Arg Tyr Thr His Val Lys
55       50           55           60
56   Asp Glu Val Arg Tyr Glu Val Asn Cys Ser Gly Ile Tyr Glu Gln Glu
57       65           70           75           80
58   Pro Leu Glu Ile Gly Lys Ser Leu Glu Ile Arg Arg Arg Asp Ile Ile
59       85           90           95
60   Asp Leu Glu Asp Asp Asp Val Val Ala Met Thr Ser Asp Cys Asp Ile
61       100          105          110
62   Tyr Gln Thr Leu Arg Gly Tyr Ala Gln Lys Leu Val Ser Lys Glu Glu
63       115          120          125
64   Lys Ser Phe Pro Ile Ala Tyr Ser Leu Val Val His Lys Asp Ala Ile
65       130          135          140
66   Met Val Glu Arg Leu Ile His Ala Ile Tyr Asn Gln His Asn Ile Tyr
67       145          150          155          160
68   Cys Ile His Tyr Asp Arg Lys Ala Pro Asp Thr Phe Lys Val Ala Met
69       165          170          175
70   Asn Asn Leu Ala Lys Cys Phe Ser Asn Ile Phe Ile Ala Ser Lys Leu
71       180          185          190
72   Glu Ala Val Glu Tyr Ala His Ile Ser Arg Leu Gln Ala Asp Leu Asn
73       195          200          205
74   Cys Leu Ser Asp Leu Leu Lys Ser Ser Ile Gln Trp Lys Tyr Val Ile
75       210          215          220
76   Asn Leu Cys Gly Gln Asp Phe Pro Leu Lys Ser Asn Phe Glu Leu Val
77       225          230          235          240
78   Ser Glu Leu Lys Lys Leu Asn Gly Ala Asn Met Leu Glu Thr Val Lys
79       245          250          255
80   Pro Pro Asn Ser Lys Leu Glu Arg Phe Thr Tyr His His Glu Leu Arg
81       260          265          270
82   Arg Val Pro Tyr Glu Tyr Val Lys Leu Pro Ile Arg Thr Asn Ile Ser
83       275          280          285
84   Lys Glu Ala Pro Pro His Asn Ile Gln Ile Phe Val Gly Ser Ala Tyr
85       290          295          300
86   Phe Val Leu Ser Gln Ala Phe Val Lys Tyr Ile Phe Asn Asn Ser Ile
87       305          310          315          320
88   Val Gln Asp Phe Phe Ala Trp Ser Lys Asp Thr Tyr Ser Pro Asp Glu
89       325          330          335
90   His Phe Trp Ala Thr Leu Ile Arg Val Pro Gly Ile Pro Gly Glu Ile
91       340          345          350
92   Ser Arg Ser Ala Gln Asp Val Ser Asp Leu Gln Ser Lys Thr Arg Leu
93       355          360          365
94   Val Lys Trp Asn Tyr Tyr Glu Gly Phe Phe Tyr Pro Ser Cys Thr Gly

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95          370          375          380
96 Ser His Leu Arg Ser Val Cys Ile Tyr Gly Ala Ala Glu Leu Arg Trp
97 385          390          395          400
98 Leu Ile Lys Asp Gly His Trp Phe Ala Asn Lys Phe Asp Ser Lys Val
99          405          410          415
100 Asp Pro Ile Leu Ile Lys Cys Leu Ala Glu Lys Leu Glu Glu Gln Gln
101          420          425          430
102 Arg Asp Trp Ile Thr Leu Pro Ser Glu Lys Leu Phe Met Asp Arg Asn
103          435          440          445
104 Leu Thr Thr Thr Ser
105          450
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 21
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Primer
113 <400> SEQUENCE: 3
114          ggtttcacccg tctccaacat a                                21
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 32
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Primer
122 <400> SEQUENCE: 4
123          cgaggatcca gaatgaagat attcaaatgt ta                        32
125 <210> SEQ ID NO: 5
126 <211> LENGTH: 31
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Primer
131 <400> SEQUENCE: 5
132          cgaggatccg caaaaagaca ttacttggt t                            31
134 <210> SEQ ID NO: 6
135 <211> LENGTH: 20
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Primer
140 <400> SEQUENCE: 6
141          tcgtaaggca cctgatactt                                20
143 <210> SEQ ID NO: 7
144 <211> LENGTH: 22
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Primer

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149	<400>	SEQUENCE: 7	
150		gagtcagtggt ggaattgaat ac	22
152	<210>	SEQ ID NO: 8	
153	<211>	LENGTH: 21	
154	<212>	TYPE: DNA	
155	<213>	ORGANISM: Artificial Sequence	
156	<220>	FEATURE:	
157	<223>	OTHER INFORMATION: Primer	
158	<400>	SEQUENCE: 8	
159		gatctctgat ttggctcagt g	21
161	<210>	SEQ ID NO: 9	
162	<211>	LENGTH: 31	
163	<212>	TYPE: DNA	
164	<213>	ORGANISM: Artificial Sequence	
165	<220>	FEATURE:	
166	<223>	OTHER INFORMATION: Primer	
167	<400>	SEQUENCE: 9	
168		agcgaattct tactatcatg atgtggtagt g	31
170	<210>	SEQ ID NO: 10	
171	<211>	LENGTH: 21	
172	<212>	TYPE: DNA	
173	<213>	ORGANISM: Artificial Sequence	
174	<220>	FEATURE:	
175	<223>	OTHER INFORMATION: Primer	
176	<400>	SEQUENCE: 10	
177		gggcagcatt tgcctagtat g	21
179	<210>	SEQ ID NO: 11	
180	<211>	LENGTH: 20	
181	<212>	TYPE: DNA	
182	<213>	ORGANISM: Artificial Sequence	
183	<220>	FEATURE:	
184	<223>	OTHER INFORMATION: Primer	
185	<400>	SEQUENCE: 11	
186		caacagtctc ctcaaccctg	20
188	<210>	SEQ ID NO: 12	
189	<211>	LENGTH: 1287	
190	<212>	TYPE: DNA	
191	<213>	ORGANISM: Human	
192	<400>	SEQUENCE: 12	
193		atgctgagga cgttgctgcg aaggagactt ttttcttata ccaccaaata ctactttatg	60
194		gttcttggtt tatccctaata cactttctcc gttttaagga ttcatcaaaa gcctgaattt	120
195		gtaagtgtca gacacttgga gcttgctggg gagaatccta gtagtgatat taattgcacc	180
196		aaagttttac aggggtgatgt aaatgaaatc caaaaggtaa agcttgagat cctaacagtg	240
197		aaatttaaaa agcgcctctg gtggacacct gacgactata taaacatgac cagtgactgt	300
198		tcttctttca tcaagagacg caaatatatt gtagaacccc ttagtaaaaga agaggcggag	360
199		tttccaatag catattctat agtggttcat cacaagattg aaatgcttga caggctgctg	420
200		agggccatct atatgcctca gaatttctat tgcgttcatg tggacacaaa atccgaggat	480
201		tcctatttag ctgcagtgat gggcatcgct tcctgtttta gtaatgtctt tgtggccagc	540
202		cgattggaga gtgtggttta tgcacgtggg agccgggttc aggctgacct caactgcatg	600

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203      aaggatctct atgcaatgag tgcaaactgg aagtacttga taaatctttg tgggatggat      660
204      ttccccatta aaaccaacct agaaattgtc aggaagctca agttgttaat gggagaaaac      720
205      aacctggaaa cggagaggat gccatcccat aaagaagaaa ggtggaagaa gcggtatgag      780
206      gtcgttaatg gaaagctgac aaacacaggg actgtcaaaa tgcttctctc actcgaaaca      840
207      cctctctttt ctggcagtgc ctacttcgtg gtcagtaggg agtatgtggg gtatgtacta      900
208      cagaatgaaa aaatccaaaa gttgatggag tgggcacaag acacatacag ccctgatgag      960
209      tatctctggg ccacatcca aaggattcct gaagtcctcg gctcactccc tgccagccat     1020
210      aagtatgac tatctgacat gcaagcagtt gccaggtttg tcaagtggca gtactttgag     1080
211      ggtgatgttt ccaagggtgc tccctaccog ccctgcgatg gagtccatgt gcgctcagtg     1140
212      tgcattttcg gagctggtga cttgaactgg atgtctgcga aacaccactt gtttgccaat     1200
213      aagtttgacg tggatgttga cctctttgcc atccagtgtt tggatgagca tttgagacac     1260
214      aaagctttgg agacattaaa aactgta                                     1287
216 <210> SEQ ID NO: 13
217 <211> LENGTH: 428
218 <212> TYPE: PRT
219 <213> ORGANISM: Human
220 <400> SEQUENCE: 13
221      Met Leu Arg Thr Leu Leu Arg Arg Arg Leu Phe Ser Tyr Pro Thr Lys
222      1          5          10          15
223      Tyr Tyr Phe Met Val Leu Val Leu Ser Leu Ile Thr Phe Ser Val Leu
224      20          25          30
225      Arg Ile His Gln Lys Pro Glu Phe Val Ser Val Arg His Leu Glu Leu
226      35          40          45
227      Ala Gly Glu Asn Pro Ser Ser Asp Ile Asn Cys Thr Lys Val Leu Gln
228      50          55          60
229      Gly Asp Val Asn Glu Ile Gln Lys Val Lys Leu Glu Ile Leu Thr Val
230      65          70          75          80
231      Lys Phe Lys Lys Arg Pro Arg Trp Thr Pro Asp Asp Tyr Ile Asn Met
232      85          90          95
233      Thr Ser Asp Cys Ser Ser Phe Ile Lys Arg Arg Lys Tyr Ile Val Glu
234      100         105         110
235      Pro Leu Ser Lys Glu Glu Ala Glu Phe Pro Ile Ala Tyr Ser Ile Val
236      115         120         125
237      Val His His Lys Ile Glu Met Leu Asp Arg Leu Leu Arg Ala Ile Tyr
238      130         135         140
239      Met Pro Gln Asn Phe Tyr Cys Val His Val Asp Thr Lys Ser Glu Asp
240      145         150         155         160
241      Ser Tyr Leu Ala Ala Val Met Gly Ile Ala Ser Cys Phe Ser Asn Val
242      165         170         175
243      Phe Val Ala Ser Arg Leu Glu Ser Val Val Tyr Ala Ser Trp Ser Arg
244      180         185         190
245      Val Gln Ala Asp Leu Asn Cys Met Lys Asp Leu Tyr Ala Met Ser Ala
246      195         200         205
247      Asn Trp Lys Tyr Leu Ile Asn Leu Cys Gly Met Asp Phe Pro Ile Lys
248      210         215         220
249      Thr Asn Leu Glu Ile Val Arg Lys Leu Lys Leu Leu Met Gly Glu Asn
250      225         230         235         240
251      Asn Leu Glu Thr Glu Arg Met Pro Ser His Lys Glu Glu Arg Trp Lys
252      245         250         255

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10084406.raw

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